

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

(i) APPLICANT: Griffith, Irwin J.  
Pollock, Joanne

(ii) TITLE OF INVENTION: Allergenic Proteins And Peptides From  
Japanese Cedar Pollen

(iii) NUMBER OF SEQUENCES: 25

## (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris  
(B) STREET: 46th Floor - 1 Liberty Place  
(C) CITY: Philadelphia  
(D) STATE: PA  
(E) COUNTRY: USA  
(F) ZIP: 19103

## (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

## (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:  
(B) FILING DATE:  
(C) CLASSIFICATION:

## (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Hohenschutz, Liza D.  
(B) REGISTRATION NUMBER: 33,712  
(C) REFERENCE/DOCKET NUMBER: IMPH-0001

## (ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (215) 568-3100  
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## (2) INFORMATION FOR SEQ ID NO:1:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1337 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(vi) ORIGINAL SOURCE:

## Patent Application US/07/730,452

54 (A) ORGANISM: *Cryptomeria japonica*  
55  
56 (ix) FEATURE:  
57 (A) NAME/KEY: CDS  
58 (B) LOCATION: 66..1187  
59  
60 (ix) FEATURE:  
61 (A) NAME/KEY: mat\_peptide  
62 (B) LOCATION: 129..1187  
63  
64  
65 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:  
66  
67 AGTCAATCTG CTCATAATCA TAGCATAGCC GTATAGAAAG AAATTCTACA CTCTGCTACC 60  
68  
69 AAAAA ATG GAT TCC CCT TGC TTA GTA GCA TTA CTG GTT TTC TCT TTT 107  
70 Met Asp Ser Pro Cys Leu Val Ala Leu Leu Val Phe Ser Phe  
71 -21 -20 -15 -10  
72  
73 GTA ATT GGA TCT TGC TTT TCT GAT AAT CCC ATA GAC AGC TGC TGG AGA 155  
74 Val Ile Gly Ser Cys Phe Ser Asp Asn Pro Ile Asp Ser Cys Trp Arg  
75 -5 1 5  
76  
77 GGA GAC TCA AAC TGG GCC CAA AAT AGA ATG AAG CTC GCA GAT TGT GCA 203  
78 Gly Asp Ser Asn Trp Ala Gln Asn Arg Met Lys Leu Ala Asp Cys Ala  
79 10 15 20 25  
80  
81 GTG GGC TTC GGA AGC TCC ACC ATG GGA GGC AAG GGA GGA GAT CTT TAT 251  
82 Val Gly Phe Gly Ser Ser Thr Met Gly Gly Lys Gly Gly Asp Leu Tyr  
83 30 35 40  
84  
85 ACG GTC ACG AAC TCA GAT GAC GAC CCT GTG AAT CCT GCA CCA GGA ACT 299  
86 Thr Val Thr Asn Ser Asp Asp Asp Pro Val Asn Pro Ala Pro Gly Thr  
87 45 50 55  
88  
89 CTG CGC TAT GGA GCA ACC CGA GAT AGG CCC CTG TGG ATA ATT TTC AGT 347  
90 Leu Arg Tyr Gly Ala Thr Arg Asp Arg Pro Leu Trp Ile Ile Phe Ser  
91 60 65 70  
92  
93 GGG AAT ATG AAT ATA AAG CTC AAA ATG CCT ATG TAC ATT GCT GGG TAT 395  
94 Gly Asn Met Asn Ile Lys Leu Lys Met Pro Met Tyr Ile Ala Gly Tyr  
95 75 80 85  
96  
97 AAG ACT TTT GAT GGC AGG GGA GCA CAA GTT TAT ATT GGC AAT GGC GGT 443  
98 Lys Thr Phe Asp Gly Arg Gly Ala Gln Val Tyr Ile Gly Asn Gly Gly  
99 90 95 100 105  
100  
101 CCC TGT GTG TTT ATC AAG AGA GTT AGC AAT GTT ATC ATA CAC GGT TTG 491  
102 Pro Cys Val Phe Ile Lys Arg Val Ser Asn Val Ile Ile His Gly Leu  
103 110 115 120  
104  
105 TAT CTG TAC GGC TGT AGT ACT AGT GTT TTG GGG AAT GTT TTG ATA AAC 539  
106 Tyr Leu Tyr Gly Cys Ser Thr Ser Val Leu Gly Asn Val Leu Ile Asn

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107				125					130				135				
108																	
109	GAG	AGT	TTT	GGG	GTG	GAG	CCT	GTT	CAT	CCT	CAG	GAT	GGC	GAT	GCT	CTT	587
110	Glu	Ser	Phe	Gly	Val	Glu	Pro	Val	His	Pro	Gln	Asp	Gly	Asp	Ala	Leu	
111				140					145				150				
112																	
113	ACT	CTG	CGC	ACT	GCT	ACA	AAT	ATT	TGG	ATT	GAT	CAT	AAT	TCT	TTC	TCC	635
114	Thr	Leu	Arg	Thr	Ala	Thr	Asn	Ile	Trp	Ile	Asp	His	Asn	Ser	Phe	Ser	
115				155					160				165				
116																	
117	AAT	TCT	TCT	GAT	GGT	CTG	GTC	GAT	GTC	ACT	CTT	ACT	TCG	ACT	GGA	GTT	683
118	Asn	Ser	Ser	Asp	Gly	Leu	Val	Asp	Val	Thr	Leu	Thr	Ser	Thr	Gly	Val	
119	170					175					180					185	
120																	
121	ACT	ATT	TCA	AAC	AAT	CTT	TTT	TTC	AAC	CAT	CAT	AAA	GTG	ATG	TTG	TTA	731
122	Thr	Ile	Ser	Asn	Asn	Leu	Phe	Phe	Asn	His	His	Lys	Val	Met	Leu	Leu	
123						190					195				200		
124																	
125	GGG	CAT	GAT	GAT	GCA	TAT	AGT	GAT	GAC	AAA	TCC	ATG	AAG	GTG	ACA	GTG	779
126	Gly	His	Asp	Asp	Ala	Tyr	Ser	Asp	Asp	Lys	Ser	Met	Lys	Val	Thr	Val	
127				205					210					215			
128																	
129	GCG	TTC	AAT	CAA	TTT	GGA	CCT	AAC	TGT	GGA	CAA	AGA	ATG	CCC	AGG	GCA	827
130	Ala	Phe	Asn	Gln	Phe	Gly	Pro	Asn	Cys	Gly	Gln	Arg	Met	Pro	Arg	Ala	
131				220					225				230				
132																	
133	CGA	TAT	GGA	CTT	GTA	CAT	GTT	GCA	AAC	AAT	AAT	TAT	GAC	CCA	TGG	ACT	875
134	Arg	Tyr	Gly	Leu	Val	His	Val	Ala	Asn	Asn	Asn	Tyr	Asp	Pro	Trp	Thr	
135				235					240				245				
136																	
137	ATA	TAT	GCA	ATT	GGT	GGG	AGT	TCA	AAT	CCA	ACC	ATT	CTA	AGT	GAA	GGG	923
138	Ile	Tyr	Ala	Ile	Gly	Gly	Ser	Ser	Asn	Pro	Thr	Ile	Leu	Ser	Glu	Gly	
139	250					255					260					265	
140																	
141	AAT	AGT	TTC	ACT	GCA	CCA	AAT	GAG	AGC	TAC	AAG	AAG	CAA	GTA	ACC	ATA	971
142	Asn	Ser	Phe	Thr	Ala	Pro	Asn	Glu	Ser	Tyr	Lys	Lys	Gln	Val	Thr	Ile	
143					270					275					280		
144																	
145	CGT	ATT	GGA	TGC	AAA	ACA	TCA	TCA	TCT	TGT	TCA	AAT	TGG	GTG	TGG	CAA	1019
146	Arg	Ile	Gly	Cys	Lys	Thr	Ser	Ser	Ser	Cys	Ser	Asn	Trp	Val	Trp	Gln	
147				285					290				295				
148																	
149	TCT	ACA	CAA	GAT	GTT	TTT	TAT	AAT	GGA	GCT	TAT	TTT	GTA	TCA	TCA	GGG	1067
150	Ser	Thr	Gln	Asp	Val	Phe	Tyr	Asn	Gly	Ala	Tyr	Phe	Val	Ser	Ser	Gly	
151				300					305				310				
152																	
153	AAA	TAT	GAA	GGG	GGT	AAT	ATA	TAC	ACA	AAG	AAA	GAA	GCT	TTC	AAT	GTT	1115
154	Lys	Tyr	Glu	Gly	Gly	Asn	Ile	Tyr	Thr	Lys	Lys	Glu	Ala	Phe	Asn	Val	
155				315				320				325					
156																	
157	GAG	AAT	GGG	AAT	GCA	ACT	CCT	CAA	TTG	ACA	AAA	AAT	GCT	GGG	GTT	TTA	1163
158	Glu	Asn	Gly	Asn	Ala	Thr	Pro	Gln	Leu	Thr	Lys	Asn	Ala	Gly	Val	Leu	
159	330					335				340					345		

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160  
161 ACA TGC TCT CTC TCT AAA CGT TGT TGATGATGCA TATATTCTAG CATGTTGTAC 1217  
162 Thr Cys Ser Leu Ser Lys Arg Cys  
163 350  
164  
165 TATCTAAATT AACATCAACA AGAAAATATA TCATGATGTA TATTGTTGTA TTGATGTCAA 1277  
166  
167 AATAAAAATG TATCTTTTAC TATTAAAAAA AAAAATGATC GATCGGACGG TACCTCTAGA 1337  
168  
169  
170  
171 (2) INFORMATION FOR SEQ ID NO:2:  
172  
173 (i) SEQUENCE CHARACTERISTICS:  
174 (A) LENGTH: 374 amino acids  
175 (B) TYPE: amino acid  
176 (D) TOPOLOGY: linear  
177  
178 (ii) MOLECULE TYPE: protein  
179  
180 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:  
181  
182 Met Asp Ser Pro Cys Leu Val Ala Leu Leu Val Phe Ser Phe Val Ile  
183 -21 -20 -15 -10  
184  
185 Gly Ser Cys Phe Ser Asp Asn Pro Ile Asp Ser Cys Trp Arg Gly Asp  
186 -5 1 5 10  
187  
188 Ser Asn Trp Ala Gln Asn Arg Met Lys Leu Ala Asp Cys Ala Val Gly  
189 15 20 25  
190  
191 Phe Gly Ser Ser Thr Met Gly Gly Lys Gly Gly Asp Leu Tyr Thr Val  
192 30 35 40  
193  
194 Thr Asn Ser Asp Asp Asp Pro Val Asn Pro Ala Pro Gly Thr Leu Arg  
195 45 50 55  
196  
197 Tyr Gly Ala Thr Arg Asp Arg Pro Leu Trp Ile Ile Phe Ser Gly Asn  
198 60 65 70 75  
199  
200 Met Asn Ile Lys Leu Lys Met Pro Met Tyr Ile Ala Gly Tyr Lys Thr  
201 80 85 90  
202  
203 Phe Asp Gly Arg Gly Ala Gln Val Tyr Ile Gly Asn Gly Gly Pro Cys  
204 95 100 105  
205  
206 Val Phe Ile Lys Arg Val Ser Asn Val Ile Ile His Gly Leu Tyr Leu  
207 110 115 120  
208  
209 Tyr Gly Cys Ser Thr Ser Val Leu Gly Asn Val Leu Ile Asn Glu Ser  
210 125 130 135  
211  
212 Phe Gly Val Glu Pro Val His Pro Gln Asp Gly Asp Ala Leu Thr Leu

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213 140 145 150 155  
214  
215 Arg Thr Ala Thr Asn Ile Trp Ile Asp His Asn Ser Phe Ser Asn Ser  
216 160 165 170  
217  
218 Ser Asp Gly Leu Val Asp Val Thr Leu Thr Ser Thr Gly Val Thr Ile  
219 175 180 185  
220  
221 Ser Asn Asn Leu Phe Phe Asn His His Lys Val Met Leu Leu Gly His  
222 190 195 200  
223  
224 Asp Asp Ala Tyr Ser Asp Asp Lys Ser Met Lys Val Thr Val Ala Phe  
225 205 210 215  
226  
227 Asn Gln Phe Gly Pro Asn Cys Gly Gln Arg Met Pro Arg Ala Arg Tyr  
228 220 225 230 235  
229  
230 Gly Leu Val His Val Ala Asn Asn Asn Tyr Asp Pro Trp Thr Ile Tyr  
231 240 245 250  
232  
233 Ala Ile Gly Gly Ser Ser Asn Pro Thr Ile Leu Ser Glu Gly Asn Ser  
234 255 260 265  
235  
236 Phe Thr Ala Pro Asn Glu Ser Tyr Lys Lys Gln Val Thr Ile Arg Ile  
237 270 275 280  
238  
239 Gly Cys Lys Thr Ser Ser Ser Cys Ser Asn Trp Val Trp Gln Ser Thr  
240 285 290 295  
241  
242 Gln Asp Val Phe Tyr Asn Gly Ala Tyr Phe Val Ser Ser Gly Lys Tyr  
243 300 305 310 315  
244  
245 Glu Gly Gly Asn Ile Tyr Thr Lys Lys Glu Ala Phe Asn Val Glu Asn  
246 320 325 330  
247  
248 Gly Asn Ala Thr Pro Gln Leu Thr Lys Asn Ala Gly Val Leu Thr Cys  
249 335 340 345  
250  
251 Ser Leu Ser Lys Arg Cys  
252 350  
253

## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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266 GAYAAAYCCNA THGAYWS 17  
267  
268 (2) INFORMATION FOR SEQ ID NO:4:  
269  
270 (i) SEQUENCE CHARACTERISTICS:  
271 (A) LENGTH: 25 base pairs  
272 (B) TYPE: nucleic acid  
273 (C) STRANDEDNESS: single  
274 (D) TOPOLOGY: linear  
275  
276  
277  
278 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:  
279  
280 GGGGAATTCAA YTGGGCNCAR AAYSG 25  
281  
282 (2) INFORMATION FOR SEQ ID NO:5:  
283  
284 (i) SEQUENCE CHARACTERISTICS:  
285 (A) LENGTH: 23 base pairs  
286 (B) TYPE: nucleic acid  
287 (C) STRANDEDNESS: single  
288 (D) TOPOLOGY: linear  
289  
290  
291 (ix) FEATURE:  
292 (A) NAME/KEY: modified\_base  
293 (B) LOCATION: 15  
294 (D) OTHER INFORMATION: /mod\_base= i  
295  
296  
297 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:  
298  
299 CTGCAGCCRT TYTCNACRTT RAA 23  
300  
301 (2) INFORMATION FOR SEQ ID NO:6:  
302  
303 (i) SEQUENCE CHARACTERISTICS:  
304 (A) LENGTH: 20 base pairs  
305 (B) TYPE: nucleic acid  
306 (C) STRANDEDNESS: single  
307 (D) TOPOLOGY: linear  
308  
309  
310 (ix) FEATURE:  
311 (A) NAME/KEY: modified\_base  
312 (B) LOCATION: 6  
313 (D) OTHER INFORMATION: /mod\_base= i  
314  
315  
316 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:  
317  
318 TTCATNCKRT TYTGNGCCCA 20

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319  
320 (2) INFORMATION FOR SEQ ID NO:7:  
321  
322 (i) SEQUENCE CHARACTERISTICS:  
323 (A) LENGTH: 25 base pairs  
324 (B) TYPE: nucleic acid  
325 (C) STRANDEDNESS: single  
326 (D) TOPOLOGY: linear  
327  
328  
329  
330 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:  
331  
332 CCTGCAGCKR TTYTGNGCCC AARTT 25  
333  
334 (2) INFORMATION FOR SEQ ID NO:8:  
335  
336 (i) SEQUENCE CHARACTERISTICS:  
337 (A) LENGTH: 18 base pairs  
338 (B) TYPE: nucleic acid  
339 (C) STRANDEDNESS: single  
340 (D) TOPOLOGY: linear  
341  
342  
343  
344 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:  
345  
346 ATGGATTCCC CTTGCTTA 18  
347  
348 (2) INFORMATION FOR SEQ ID NO:9:  
349  
350 (i) SEQUENCE CHARACTERISTICS:  
351 (A) LENGTH: 26 base pairs  
352 (B) TYPE: nucleic acid  
353 (C) STRANDEDNESS: single  
354 (D) TOPOLOGY: linear  
355  
356  
357  
358 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:  
359  
360 GGGAATTCGA TAATCCATA GACAGC 26  
361  
362 (2) INFORMATION FOR SEQ ID NO:10:  
363  
364 (i) SEQUENCE CHARACTERISTICS:  
365 (A) LENGTH: 17 base pairs  
366 (B) TYPE: nucleic acid  
367 (C) STRANDEDNESS: single  
368 (D) TOPOLOGY: linear  
369  
370  
371

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372 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

373

374 ATGCCTATGT ACATTGC

17

375

376 (2) INFORMATION FOR SEQ ID NO:11:

377

378 (i) SEQUENCE CHARACTERISTICS:

379 (A) LENGTH: 17 base pairs

380 (B) TYPE: nucleic acid

381 (C) STRANDEDNESS: single

382 (D) TOPOLOGY: linear

383

384

385

386 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

387

388 GCAATGTACA TAGGCAT

17

389

390 (2) INFORMATION FOR SEQ ID NO:12:

391

392 (i) SEQUENCE CHARACTERISTICS:

393 (A) LENGTH: 18 base pairs

394 (B) TYPE: nucleic acid

395 (C) STRANDEDNESS: single

396 (D) TOPOLOGY: linear

397

398

399

400 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

401

402 TCCAATTCTT CTGATGGT

18

403

404 (2) INFORMATION FOR SEQ ID NO:13:

405

406 (i) SEQUENCE CHARACTERISTICS:

407 (A) LENGTH: 18 base pairs

408 (B) TYPE: nucleic acid

409 (C) STRANDEDNESS: single

410 (D) TOPOLOGY: linear

411

412

413

414 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

415

416 TTTTGTCAAT TGAGGAGT

18

417

418 (2) INFORMATION FOR SEQ ID NO:14:

419

420 (i) SEQUENCE CHARACTERISTICS:

421 (A) LENGTH: 30 base pairs

422 (B) TYPE: nucleic acid

423 (C) STRANDEDNESS: single

424 (D) TOPOLOGY: linear



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425  
426  
427  
428 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:  
429  
430 CCTGCAGAAG CTTTCATCAAC AACGTTTAGA 30  
431  
432 (2) INFORMATION FOR SEQ ID NO:15:  
433  
434 (i) SEQUENCE CHARACTERISTICS:  
435 (A) LENGTH: 18 base pairs  
436 (B) TYPE: nucleic acid  
437 (C) STRANDEDNESS: single  
438 (D) TOPOLOGY: linear  
439  
440  
441  
442 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:  
443  
444 TAGAACTCCA GTCGAAGT 18  
445  
446 (2) INFORMATION FOR SEQ ID NO:16:  
447  
448 (i) SEQUENCE CHARACTERISTICS:  
449 (A) LENGTH: 17 base pairs  
450 (B) TYPE: nucleic acid  
451 (C) STRANDEDNESS: single  
452 (D) TOPOLOGY: linear  
453  
454  
455  
456 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:  
457  
458 TAGCTCTCAT TTGGTGC 17  
459  
460 (2) INFORMATION FOR SEQ ID NO:17:  
461  
462 (i) SEQUENCE CHARACTERISTICS:  
463 (A) LENGTH: 18 base pairs  
464 (B) TYPE: nucleic acid  
465 (C) STRANDEDNESS: single  
466 (D) TOPOLOGY: linear  
467  
468  
469  
470 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:  
471  
472 TATGCAATTG GTGGGAGT 18  
473  
474 (2) INFORMATION FOR SEQ ID NO:18:  
475  
476 (i) SEQUENCE CHARACTERISTICS:  
477 (A) LENGTH: 20 amino acids

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478 (B) TYPE: amino acid  
479 (D) TOPOLOGY: linear  
480  
481 (ii) MOLECULE TYPE: peptide  
482  
483 (v) FRAGMENT TYPE: N-terminal  
484  
485 (vi) ORIGINAL SOURCE:  
486 (A) ORGANISM: *Cryptomeria japonica*  
487  
488 (ix) FEATURE:  
489 (A) NAME/KEY: Modified-site  
490 (B) LOCATION: 7  
491 (D) OTHER INFORMATION: /note= "the amino acid at position  
492 7 is Ser, Cys, Thr, or His"  
493  
494  
495 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:  
496  
497 Asp Asn Pro Ile Asp Ser Xaa Trp Arg Gly Asp Ser Asn Trp Ala Gln  
498 1 5 10 15  
499  
500 Asn Arg Met Lys  
501 20  
502  
503 (2) INFORMATION FOR SEQ ID NO:19:  
504  
505 (i) SEQUENCE CHARACTERISTICS:  
506 (A) LENGTH: 16 amino acids  
507 (B) TYPE: amino acid  
508 (D) TOPOLOGY: linear  
509  
510 (ii) MOLECULE TYPE: peptide  
511  
512 (v) FRAGMENT TYPE: internal  
513  
514 (vi) ORIGINAL SOURCE:  
515 (A) ORGANISM: *Cryptomeria japonica*  
516  
517  
518 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:  
519  
520 Glu Ala Phe Asn Val Glu Asn Gly Asn Ala Thr Pro Gln Leu Thr Lys  
521 1 5 10 15  
522  
523  
524 (2) INFORMATION FOR SEQ ID NO:20:  
525  
526 (i) SEQUENCE CHARACTERISTICS:  
527 (A) LENGTH: 30 base pairs  
528 (B) TYPE: nucleic acid  
529 (C) STRANDEDNESS: single  
530 (D) TOPOLOGY: linear

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531  
532  
533  
534 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:  
535  
536 GGGTCTAGAG GTACCGTCCG ATCGATCATT 30  
537  
538 (2) INFORMATION FOR SEQ ID NO:21:  
539  
540 (i) SEQUENCE CHARACTERISTICS:  
541 (A) LENGTH: 20 base pairs  
542 (B) TYPE: nucleic acid  
543 (C) STRANDEDNESS: single  
544 (D) TOPOLOGY: linear  
545  
546  
547  
548 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:  
549  
550 GGGTCTAGAG GTACCGTCCG 20  
551  
552 (2) INFORMATION FOR SEQ ID NO:22:  
553  
554 (i) SEQUENCE CHARACTERISTICS:  
555 (A) LENGTH: 13 base pairs  
556 (B) TYPE: nucleic acid  
557 (C) STRANDEDNESS: single  
558 (D) TOPOLOGY: linear  
559  
560  
561  
562 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:  
563  
564 AATGATCGAT GCT 13  
565  
566 (2) INFORMATION FOR SEQ ID NO:23:  
567  
568 (i) SEQUENCE CHARACTERISTICS:  
569 (A) LENGTH: 21 base pairs  
570 (B) TYPE: nucleic acid  
571 (C) STRANDEDNESS: single  
572 (D) TOPOLOGY: linear  
573  
574  
575  
576 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:  
577  
578 GGAATTCTCT AGACTGCAGG T 21  
579  
580 (2) INFORMATION FOR SEQ ID NO:24:  
581  
582 (i) SEQUENCE CHARACTERISTICS:  
583 (A) LENGTH: 35 base pairs

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584 (B) TYPE: nucleic acid  
585 (C) STRANDEDNESS: single  
586 (D) TOPOLOGY: linear  
587  
588  
589

590 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

591  
592 GGAATTCTCT AGACTGCAGG TTTTTTTTTT TTTT  
593

35

594 (2) INFORMATION FOR SEQ ID NO:25:

595  
596 (i) SEQUENCE CHARACTERISTICS:  
597 (A) LENGTH: 5 amino acids  
598 (B) TYPE: amino acid  
599 (D) TOPOLOGY: linear  
600

601 (ii) MOLECULE TYPE: peptide

602  
603 (v) FRAGMENT TYPE: N-terminal  
604

605 (vi) ORIGINAL SOURCE:  
606 (A) ORGANISM: Juniperus sabinoides  
607

608  
609 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

610  
611 Asp Asn Pro Ile Asp  
612 1 5

PAGE: 1

SEQUENCE VERIFICATION REPORT  
PATENT APPLICATION US/07/730,452

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TIME: 15:01:09

LINE ERROR

ORIGINAL TEXT

PAGE: 1

SEQUENCE MISSING ITEM REPORT  
PATENT APPLICATION US/07/730,452

DATE: 07/22/91  
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MANDATORY IDENTIFIER THAT WAS NOT FOUND

PRIOR APPLICATION DATA  
APPLICATION NUMBER  
FILING DATE

PAGE: 1

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